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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
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09/441,242 11/16/99 RUSSO

G 8666-008-999

020583
PENNIE AND EDMONDS
1155 AVENUE OF THE AMERICAS
NEW YORK NY 10036-2711

HM12/1010

EXAMINER

LEFFERS JR, G

ART UNIT

PAPER NUMBER

1636

DATE MAILED:

10/10/01

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks



UNITED STATES PATENT AND TRADEMARK OFFICE

COMMISSIONER FOR PATENTS
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APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.
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EXAMINER

Gerald G. Leffers Jr.

ART UNIT	PAPER
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1636

11

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents

The communication filed 7-16-01 is not fully responsive to the Office communication mailed 1-16-01 for the reason(s) set forth on the attached Notice To Comply With The Sequence Rules or CFR Diskette Problem Report. Applicant must comply with the requirements of the sequences rules (37 CFR 1.821 – 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Since the reply appears to a bona fide attempt to comply with the requirements of the sequence rules (37 CFR 1.821 – 1.825), applicant is given a **TIME PERIOD of ONE (1) MONTH** from the mailing date of this communication within which to correct the deficiency so as to comply with the sequence rules (37 CFR 1.821 – 1.825) in order to avoid abandonment of the application under 37 CFR 1.821 (g). EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

Any inquiry concerning this communication should be directed to Examiner **Gerald G. Leffers Jr.**, Art Unit 1636, whose telephone number is (703) 308-6232.

Any inquiry of a general nature or relating to the status of this application, or relating to attachments to this office action, should be directed to the Patent Analyst Zeta Adams, whose telephone number is (703) 305-3291.

ADD
ggl

DAVID GUZO
PRIMARY EXAMINER

Notice to Comply

Application No.

09/441,242

Examiner

Gerald G. Leffers Jr.

Applicant(s)

RUSSO ET AL.

Art Unit

1636

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

Applicant Must Provide:

- ☐ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☐ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

G. Letters

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



09/441,242
Attach Paper #11
file copy

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/441,242
Source: OIP
Date Processed by STIC: 7/26/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/441,242

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) 2 missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/441,242

DATE: 07/26/2001

TIME: 15:22:26

Input Set : A:\8666-008seqlist.txt

Output Set: N:\CRF3\07262001\I441242.raw

pp. 215
Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Russo, Giandomenico et al.
 5 <120> TITLE OF INVENTION: TCL-1 Gene and Protein and Related Methods and Compositions
 7 <130> FILE REFERENCE: 8666-008
 9 <140> CURRENT APPLICATION NUMBER: 09/441,242
 10 <141> CURRENT FILING DATE: 1999-11-16
 12 <160> NUMBER OF SEQ ID NOS: 12
 14 <170> SOFTWARE: PatentIn version 3.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 1324
 18 <212> TYPE: DNA
 C--> 19 <213> ORGANISM: Artificial
 21 <220> FEATURE:
 22 <223> OTHER INFORMATION: cDNA sequence of TCL-1
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (49)..(387)
 28 <400> SEQUENCE: 1
 29 cttgagaggc tctggctctt gcttcttagg cggcccgagg acgccatg gcc gag tgc 57
 30 Ala Glu Cys
 31 1
 33 ccg aca ctc ggg gag gca gtc acc gac cac ccg gac cgc ctg tgg gcc 105
 34 Pro Thr Leu Gly Glu Ala Val Thr Asp His Pro Asp Arg Leu Trp Ala
 35 5 10 15
 37 tgg gag aag ttc gtg tat ttg gac gag aag cag cac gcc tgg ctg ccc 153
 38 Trp Glu Lys Phe Val Tyr Leu Asp Glu Lys Gln His Ala Trp Leu Pro
 39 20 25 30 35
 41 tta acc atc gag ata aag gat agg tta cag tta cgg gtg ctc ttg cgt 201
 42 Leu Thr Ile Glu Ile Lys Asp Arg Leu Gln Leu Arg Val Leu Leu Arg
 43 40 45 50
 45 cgg gaa gac gtc gtc ctg ggg agg cct atg acc ccc acc cag ata ggc 249
 46 Arg Glu Asp Val Val Leu Gly Arg Pro Met Thr Pro Thr Gln Ile Gly
 47 55 60 65
 49 cca agc ctg ctg cct atc atg tgg cag ctc tac cct gat gga cga tac 297
 50 Pro Ser Leu Leu Pro Ile Met Trp Gln Leu Tyr Pro Asp Gly Arg Tyr
 51 70 75 80
 53 cga tcc tca gac tcc agt ttc tgg cgc tta gtg tac cac atc aag att 345
 54 Arg Ser Ser Asp Ser Ser Phe Trp Arg Leu Val Tyr His Ile Lys Ile
 55 85 90 95
 57 gac ggc gtg gag gac atg ctt ctc gag ctg ctg cca gat gac 387
 58 Asp Gly Val Glu Asp Met Leu Leu Glu Leu Leu Pro Asp Asp
 59 100 105 110
 61 tgatgtatgg tcttggcagc acctgtctcc ttccacccca gggcctgagc ctggccagcc 447
 63 tacaatgggg atgttggtt tctgttcacc ttctgttact atgcctgtgt cttctccacc 507
 65 acgctggggg ctgggaggaa tggacagaca gaggatgagc tctacccagg gcctgcagga 567
 67 cctgcctgta gccactctg ctgccttag cactaccact cctgccaagg aggattccat 627
 69 ttggcagagc ttcttccagg tgcccagcta tacctgtgcc tcggcttttc tcagctggat 687
 71 gatggtcttc agcctctttc tgtcccttct gtccctcaca gcactagtat ttcattgtgc 747

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/441,242

DATE: 07/26/2001

TIME: 15:22:26

Input Set : A:\8666-008seqlist.txt

Output Set: N:\CRF3\07262001\I441242.raw

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73 acaccactc agctcgtga acttgtaga acacagccga ttcacctgag oaggacctct 807
75 gaaacctgga accagtggc tcacatggg ctacgcctgc atgtaaacac gcctgcaaac 867
77 gctgcctgcc ggtaaacacg cctgcaaacg ctgcctgccc gtaaacacgc ctgcaaacgc 927
79 tgctgcccc cacaggttca cgtgcagctc aaggaaaggc ctgaaaggag cccttatctg 987
81 tgctcaggac tcagaagcct ctgggtcagt ggtccacatc ccgggacgca gcaggaggcc 1047
83 aggcggcgga gccctgtgga tgagccctca gaaccttggt cttgcccacg tggaaaaggg 1107
85 atagaggttg ggtttcccc ctttatagat ggtcacgcac ctgggtgtta caaagttgta 1167
87 tgtggcatga atactttttg taatgattga ttaaattgaa gatagtttat ctaacttcgt 1227
89 gcgcaatcag cttctatcct tgacttagat tctggtggag agaagtgaga ataggcagcc 1287
91 cccaaataaa aatatattcat ggaaaaaaa aaaaaaa 1324

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94 <210> SEQ ID NO: 2

95 <211> LENGTH: 113

96 <212> TYPE: PRT

C--> 97 <213> ORGANISM: Artificial

W--> 99 <220> FEATURE:

W--> 99 <223> OTHER INFORMATION:

99 <400> SEQUENCE: 2

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101 Ala Glu Cys Pro Thr Leu Gly Glu Ala Val Thr Asp His Pro Asp Arg
102 1 5 10 15
105 Leu Trp Ala Trp Glu Lys Phe Val Tyr Leu Asp Glu Lys Gln His Ala
106 20 25 30
109 Trp Leu Pro Leu Thr Ile Glu Ile Lys Asp Arg Leu Gln Leu Arg Val
110 35 40 45
113 Leu Leu Arg Arg Glu Asp Val Val Leu Gly Arg Pro Met Thr Pro Thr
114 50 55 60
117 Gln Ile Gly Pro Ser Leu Leu Pro Ile Met Trp Gln Leu Tyr Pro Asp
118 65 70 75 80
121 Gly Arg Tyr Arg Ser Ser Asp Ser Ser Phe Trp Arg Leu Val Tyr His
122 85 90 95
125 Ile Lys Ile Asp Gly Val Glu Asp Met Leu Leu Glu Leu Leu Pro Asp
126 100 105 110

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129 Asp

133 <210> SEQ ID NO: 3

134 <211> LENGTH: 560

135 <212> TYPE: DNA

Q--> 136 <213> ORGANISM: Artificial

138 <220> FEATURE:

139 <223> OTHER INFORMATION: genomic sequence of TCL-1

141 <400> SEQUENCE: 3

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142 gtcgactgtg agttcccagc agaggcccag agtcccgggt cggcagccga gggaagcggg 60
144 ggggtcttcc agaagaagaa agggccaagg tcaccccggt gcctctccag cagcagcaga 120
146 gggcggcggg cggtgtcgtc gctggccggg gcctcgagga aggcgcgggc cagctggggc 180
148 cgggtctgcg ttcccaggag ctgccaccgt tccaggagc aagtcaggcc gggacgttag 240
150 cgctgcgcg ggacctcac ttgccaccaa ggacctcaca aacctcgccc catccttagc 300
152 gcctgcgcg gacctcact tgccaccaag accccacaa accccgcccc atcctgcctt 360
154 acgccccgcc ccaaggtcgt tctcccgaac cggggtcccg cccaagacc gtctcccgcc 420
156 cccgcgcgtt ggtggcggcc gcatgctgcc cgatatataa ggtcgggccc cacatcccag 480
158 ggaccagcga gcggccttga gaggctcttg ctcttgcttc ttaggcggcc cgaggacgcc 540
160 atggccgagt gcccgacact

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/441,242

DATE: 07/26/2001

TIME: 15:22:26

Input Set : A:\8666-008seqlist.txt

Output Set: N:\CRF3\07262001\I441242.raw

163 <210> SEQ ID NO: 4
 164 <211> LENGTH: 108
 165 <212> TYPE: PRT
 166 <213> ORGANISM: Artificial
 168 <220> FEATURE:
 169 <223> OTHER INFORMATION: MTCPl protein
 171 <220> FEATURE:
 172 <221> NAME/KEY: site
 173 <222> LOCATION: (1)..(108)
 174 <223> OTHER INFORMATION: Xaa = any amino acid
 177 <400> SEQUENCE: 4
 179 Met Ala Gly Glu Asp Val Gly Ala Pro Pro Asp His Leu Trp Val His
 180 1 5 10 15
 182 Gln Glu Gly Ile Tyr Arg Asp Glu Tyr Gln Arg Thr Trp Val Ala Val
 183 20 25 30
 185 Val Glu Glu Glu Thr Ser Phe Leu Arg Ala Arg Val Gln Gln Ile Gln
 186 35 40 45
 188 Val Pro Leu Gly Asp Ala Ala Arg Pro Ser His Leu Leu Thr Ser Gln
 189 50 55 60
 191 Leu Pro Leu Met Trp Gln Leu Tyr Pro Glu Glu Arg Tyr Met Asp Asn
 192 65 70 75 80
 194 Asn Ser Arg Leu Trp Gln Ile Gln His His Leu Met Val Arg Gly Val
 195 85 90 95
 197 Gln Glu Leu Leu Leu Lys Leu Leu Pro Asp Asp Xaa
 198 100 105
 200 <210> SEQ ID NO: 5
 201 <211> LENGTH: 4922
 202 <212> TYPE: DNA
 203 <213> ORGANISM: Artificial
 205 <220> FEATURE:
 206 <223> OTHER INFORMATION: genomic DNA of TCL-1
 208 <220> FEATURE:
 209 <221> NAME/KEY: modified_base
 210 <222> LOCATION: (1)..(4922)
 211 <223> OTHER INFORMATION: m = a or c
 212 r = a or g
 213 w = a or t
 214 s = c or g
 217 <220> FEATURE:
 218 <221> NAME/KEY: modified_base
 219 <222> LOCATION: (1)..(4922)
 220 <223> OTHER INFORMATION: y = c or t
 221 k = g or t
 222 v = a, c or g
 223 h = a, c or t
 226 <220> FEATURE:
 227 <221> NAME/KEY: modified_base
 228 <222> LOCATION: (1)..(4922)
 229 <223> OTHER INFORMATION: d = a, g or t

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/441,242

DATE: 07/26/2001

TIME: 15:22:26

Input Set : A:\8666-008seqlist.txt

Output Set: N:\CRF3\07262001\I441242.raw

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230      b = c, g, or t
231      n = a, c, g, or t
234 <400> SEQUENCE: 5
235 gtcgacttgt gakttyccmag magaggccca gaagtcccgg tccggcaaag cggaggggaa      60
237 gcgggggggg ttttccaaga agaagaaagg gcccaagggt caacccccgg tgccttctcc      120
239 agcagcaagc aagagggcgg cgggtcgggt gtcgctgctg gccggggccc tccgaggaaa      180
241 ggcgcggrcc agctggggcc ggggtctgctg tcccaggagc tgccaccgtt ccaggaggca      240
243 agtcaggccg ggacgttagc gcctgcgcgg gacctcact tgccaccaag rmccccacaa      300
245 acccgccecc atcctgyctt acgccccgcc ccaaggtcgg ttctccccga cccgggggtc      360
W--> 247 ccgcccccaa ggnccgtcct ccccgceccc gccgsttggg ggcggccgca tgetgcccgg      420
249 atataaaggg tcggccccac atcccaggga ccagcgagcg gccttgagag gctctggctc      480
251 ttgctttctta ggcgggccga ggacgccatg gccgagtgcc cgacactcgg ggaaggcagtc      540
253 accgaccacc cggaccgcct cttggcgctg gagaagttcg tgtatttggg cgagaagcag      600
255 macgcctgcc tgcccttaac catcgaggtg caaccacct tggagcggat ggcgargcag      660
W--> 257 cagggggcasc ccctgggagc ttgggatncc ctaggaaggg cgaggactca aggagcactc      720
259 actatggggc agggaggatc ccccacagat kaagccactt ttggagcggg scctctkgagg      780
261 gatgaatagg agttcctcca ggcagggaag aagggtggga aaaccccaaa ggaatgtcgg      840
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265 ttctgggctt cggggctcta atccttaaaa atgggtatct ctaagtgact catccatatg      960
267 gccgattatc ggaatcatct caggtgggtc ccagaaatct gtatttttaa aaagaaccw      1020
269 cmacagttta ggggtccaacc caggcataac caaacactg gcctaagagt tgtgaagtat      1080
271 tttcccacct accctctggg ctttatttaa gamaaccaa ttaacaagt gatgtcgtag      1140
W--> 273 tataagcgcc ggtantkgaa ycaatattga cttttttaat gtgtgatgcc ttaagatggg      1200
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281 agtgttgayt gtgtctctac agatgggaaa ctgaggcaca cmaaagtac atttgtccga      1440
283 ggtaagattg ctagtaggta atgggggttg aattctaggg tcttaaccac cacaaaatct      1500
285 gcattttttt tggcatttca attttttaaa tatgttttta ctttaaaaaat caagttaaatt      1560
287 acttaacttt ttaaaatcaa aatttgaaga aataatttga agattcagtg gatttctttt      1620
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293 agattttgcc tcacatcatt gaaaaggcca gcawtctttt tctctctttc tttctttgkt      1800
295 gttttttttt tttcctgtag awacagggtc tcgctctgtg acccaggctg gtctyaaact      1860
297 cctggcctca agcgatcctc ctgcctctgc cttccaaagc actggaatta caagtgtgag      1920
299 ccgctgcaac ccgccagaaa aaagtgtgcc tttcatggcc ctgtctgggt ggctagacac      1980
301 gtgtgtgtgc tgggtgctct ggcccagcca gagttccctg agaggagcat gcatggccta      2040
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W--> 305 gatgggtgga tgsctgscag ggagggatc cgggtktcct gcgcctggag aancctgcc      2160
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W--> 309 gttnnnggtg ctcttgctc ggaagacgt cgtccctggg aggcctatga cccccacna      2280
311 gataggccca agcctgctgc ctatcatgtg gcagctctac cctgatggac gataccgatc      2340
313 ctcagactcc agtttctgic gcttagtgta ccacatcaag gtgagtgtct ttctcccaga      2400
315 ggtccatcgg ktgatcttgg gtttccctc cymatgtct gsccttagtg gtttaycttc      2460
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325 tacctgctgt ttccagctag ggaagscsc aggagttagg aatggaggga gtggagggtc      2760

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/441,242

DATE: 07/26/2001
TIME: 15:22:26

Input Set : A:\8666-008seqlist.txt
Output Set: N:\CRF3\07262001\I441242.raw

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402 <210> SEQ ID NO: 6

403 <211> LENGTH: 20

404 <212> TYPE: DNA

OK> 405 <213> ORGANISM: Artificial

407 <220> FEATURE:

408 <223> OTHER INFORMATION: p9A primer

410 <400> SEQUENCE: 6

411 tgctgccaga tgactgatgt

20

414 <210> SEQ ID NO: 7

415 <211> LENGTH: 20

416 <212> TYPE: DNA

OK> 417 <213> ORGANISM: Artificial

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

f9f →

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/441,242

DATE: 07/26/2001

TIME: 15:22:27

Input Set : A:\8666-008seqlist.txt

Output Set: N:\CRF3\07262001\I441242.raw

L:19 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:97 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:99 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:99 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:136 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:166 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:197 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:203 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:305 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:307 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:309 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:391 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:393 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:397 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:405 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:417 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:429 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:441 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:453 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:465 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:477 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12